

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-30.rni.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:47:09 ; Search time 5.02867 Seconds
(without alignments)
8558.022 Million cell updates/sec

Title: US-08-783-734D-30
Perfect score: 23
Sequence: 1 tgttatatctggttattgaatgg 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	23	100.0	2868	3 US-08-780-562-8	Sequence 8, Appli
2	23	100.0	3097	2 US-08-599-455B-1	Sequence 1, Appli
3	23	100.0	3097	3 US-09-069-781B-1	Sequence 1, Appli
4	23	100.0	3097	3 US-09-137-132-1	Sequence 1, Appli
5	23	100.0	3097	3 US-08-864-564A-1	Sequence 1, Appli
6	23	100.0	3097	3 US-09-094-410-1	Sequence 1, Appli

	7	23	100.0	3097	3	US-08-708-123D-1	Sequence 1, Appli
	8	23	100.0	3097	3	US-08-583-153A-1	Sequence 1, Appli
	9	23	100.0	3097	3	US-08-570-142D-1	Sequence 1, Appli
	10	23	100.0	3097	3	US-08-638-524B-1	Sequence 1, Appli
	11	23	100.0	3097	4	US-09-950-149-1	Sequence 1, Appli
	12	23	100.0	3495	3	US-08-827-962-17	Sequence 17, Appl
	13	23	100.0	3650	3	US-08-837-635-5	Sequence 5, Appli
	14	23	100.0	3650	3	US-08-837-635-7	Sequence 7, Appli
	15	23	100.0	3650	3	US-08-827-962-16	Sequence 16, Appl
	16	23	100.0	3650	3	US-08-803-346-2	Sequence 2, Appli
	17	23	100.0	3854	2	US-08-599-455B-42	Sequence 42, Appl
	18	23	100.0	3854	3	US-09-069-781B-42	Sequence 42, Appl
	19	23	100.0	3854	3	US-09-137-132-42	Sequence 42, Appl
	20	23	100.0	3854	3	US-08-864-564A-42	Sequence 42, Appl
	21	23	100.0	3854	3	US-09-094-410-42	Sequence 42, Appl
	22	23	100.0	3854	3	US-08-708-123D-42	Sequence 42, Appl
	23	23	100.0	3854	3	US-08-638-524B-42	Sequence 42, Appl
	24	23	100.0	3854	4	US-09-950-149-42	Sequence 42, Appl
c	25	19.8	86.1	3018	3	US-09-949-016-4756	Sequence 4756, Ap
c	26	19.8	86.1	52494	3	US-09-949-016-16498	Sequence 16498, A
	27	18.8	81.7	123	3	US-09-313-294A-1350	Sequence 1350, Ap
	28	17.8	77.4	601	3	US-09-949-001-334	Sequence 334, App
	29	17.8	77.4	312957	3	US-09-949-001-31	Sequence 31, Appl
	30	17.8	77.4	312972	3	US-09-949-001-34	Sequence 34, Appl
c	31	17.2	74.8	543	3	US-09-248-796A-7493	Sequence 7493, Ap
	32	17.2	74.8	588	3	US-09-248-796A-3595	Sequence 3595, Ap
	33	17.2	74.8	599	3	US-09-917-254-20	Sequence 20, Appl
	34	17.2	74.8	599	4	US-09-880-107-3826	Sequence 3826, Ap
	35	17.2	74.8	601	3	US-09-949-016-56677	Sequence 56677, A
	36	17.2	74.8	150032	3	US-09-949-016-14321	Sequence 14321, A
	37	17.2	74.8	636591	3	US-09-949-016-11808	Sequence 11808, A
	38	17.2	74.8	636591	3	US-09-949-016-13388	Sequence 13388, A
	39	17.2	74.8	1664976	3	US-08-916-421B-1	Sequence 1, Appli
	40	17.2	74.8	1664976	3	US-09-692-570-1	Sequence 1, Appli
c	41	16.8	73.0	601	3	US-09-949-002-8614	Sequence 8614, Ap
c	42	16.8	73.0	2088	3	US-09-134-001C-1504	Sequence 1504, Ap
c	43	16.8	73.0	2265	3	US-09-710-279-1295	Sequence 1295, Ap
c	44	16.8	73.0	2982	3	US-09-710-279-4062	Sequence 4062, Ap
c	45	16.8	73.0	3041	3	US-09-710-279-4193	Sequence 4193, Ap

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:48:31 ; Search time 37.8753 Seconds
(without alignments)
7461.730 Million cell updates/sec

Title: US-08-783-734D-30
Perfect score: 23
Sequence: 1 tgttatatcttggttattgaatgg 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

1	23	100.0	2679	6	US-10-278-733-14	Sequence 14, Appl
2	23	100.0	2868	2	US-08-779-457-8	Sequence 8, Appli
3	23	100.0	2868	6	US-10-214-802-8	Sequence 8, Appli
4	23	100.0	2868	9	US-10-921-710-8	Sequence 8, Appli
5	23	100.0	2868	15	US-11-192-219-8	Sequence 8, Appli
6	23	100.0	3097	6	US-10-079-625-1	Sequence 1, Appli
7	23	100.0	3097	16	US-11-202-330-1	Sequence 1, Appli
8	23	100.0	3489	6	US-10-278-733-18	Sequence 18, Appl
9	23	100.0	3656	6	US-10-226-579-1	Sequence 1, Appli
10	23	100.0	3799	16	US-11-136-527-2058	Sequence 2058, Ap
11	23	100.0	3854	6	US-10-079-625-42	Sequence 42, Appl
12	23	100.0	3854	16	US-11-202-330-42	Sequence 42, Appl
c 13	19.8	86.1	598	4	US-09-925-065A-659704	Sequence 659704,
c 14	19.8	86.1	598	5	US-09-925-065A-659704	Sequence 659704,
c 15	19.8	86.1	610	4	US-09-925-065A-571055	Sequence 571055,
c 16	19.8	86.1	610	5	US-09-925-065A-571055	Sequence 571055,
c 17	19.8	86.1	616	12	US-10-301-480-292735	Sequence 292735,
c 18	19.8	86.1	616	12	US-10-301-480-906144	Sequence 906144,
19	19.8	86.1	620	4	US-09-925-065A-204616	Sequence 204616,
20	19.8	86.1	620	5	US-09-925-065A-204616	Sequence 204616,
c 21	19.8	86.1	6021	3	US-09-819-247-1	Sequence 1, Appli
c 22	19.8	86.1	6021	8	US-10-428-225-1	Sequence 1, Appli
c 23	19.8	86.1	6021	10	US-10-450-763-14985	Sequence 14985, A
c 24	19.8	86.1	6021	12	US-10-960-414-487	Sequence 487, App
c 25	19.8	86.1	100596	10	US-10-737-082-92	Sequence 92, Appl
c 26	19.8	86.1	100596	10	US-10-765-790-92	Sequence 92, Appl
27	18.8	81.7	1748	8	US-10-424-599-17613	Sequence 17613, A
c 28	18.4	80.0	588	12	US-10-301-480-479059	Sequence 479059,
c 29	18.4	80.0	588	12	US-10-301-480-1092468	Sequence 1092468,
c 30	18.4	80.0	596	4	US-09-925-065A-413011	Sequence 413011,
c 31	18.4	80.0	596	5	US-09-925-065A-413011	Sequence 413011,
32	18.4	80.0	5763	7	US-10-311-455-1262	Sequence 1262, Ap
c 33	18.2	79.1	168	9	US-10-425-115-35044	Sequence 35044, A
34	18.2	79.1	288	9	US-10-425-115-162806	Sequence 162806,
c 35	18.2	79.1	500	4	US-09-925-065A-165765	Sequence 165765,
c 36	18.2	79.1	500	5	US-09-925-065A-165765	Sequence 165765,
c 37	18.2	79.1	508	12	US-10-301-480-258037	Sequence 258037,
c 38	18.2	79.1	508	12	US-10-301-480-871446	Sequence 871446,
39	18.2	79.1	1109	8	US-10-425-114-14290	Sequence 14290, A
40	18.2	79.1	1201	9	US-10-425-115-156297	Sequence 156297,
41	18.2	79.1	3673778	7	US-10-312-841-1	Sequence 1, Appli
c 42	17.8	77.4	433	4	US-09-925-065A-665207	Sequence 665207,
c 43	17.8	77.4	433	5	US-09-925-065A-665207	Sequence 665207,
c 44	17.8	77.4	463	8	US-10-767-701-11953	Sequence 11953, A
c 45	17.8	77.4	565	4	US-09-925-065A-631937	Sequence 631937,

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:57:54 ; Search time 3.35245 Seconds
(without alignments)
8112.698 Million cell updates/sec

Title: US-08-783-734D-30
Perfect score: 23
Sequence: 1 tgttatatctggttattgaatgg 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
c 1	19.8	86.1	6021	7	US-11-266-748A-32165 Sequence 32165, A
c 2	19.8	86.1	6021	7	US-11-266-748A-32166 Sequence 32166, A
c 3	19.8	86.1	6021	7	US-11-266-748A-32167 Sequence 32167, A
c 4	18.8	81.7	1757	6	US-10-953-349-18576 Sequence 18576, A
c 5	18.8	81.7	1788	7	US-11-216-545-5800 Sequence 5800, Ap
c 6	17.8	77.4	1472	6	US-10-953-349-29147 Sequence 29147, A
7	17.2	74.8	482	7	US-11-266-748A-169065 Sequence 169065,
8	17.2	74.8	635	7	US-11-266-748A-54489 Sequence 54489, A

	9	17.2	74.8	640	7	US-11-266-748A-263107	Sequence 263107,
c	10	17.2	74.8	640	7	US-11-266-748A-323624	Sequence 323624,
	11	17.2	74.8	752	7	US-11-266-748A-362030	Sequence 362030,
	12	17.2	74.8	752	7	US-11-266-748A-387811	Sequence 387811,
c	13	17.2	74.8	752	7	US-11-266-748A-445409	Sequence 445409,
	14	17.2	74.8	945	7	US-11-266-748A-188794	Sequence 188794,
	15	17.2	74.8	961	7	US-11-266-748A-397745	Sequence 397745,
c	16	17.2	74.8	961	7	US-11-266-748A-468791	Sequence 468791,
	17	17.2	74.8	1094	7	US-11-266-748A-73574	Sequence 73574, A
c	18	17.2	74.8	1094	7	US-11-266-748A-126385	Sequence 126385,
	19	17.2	74.8	6432	7	US-11-217-529-82021	Sequence 82021, A
	20	17.2	74.8	11429	6	US-10-517-441-479	Sequence 479, App
	21	17.2	74.8	11429	6	US-10-517-441-753	Sequence 753, App
c	22	16.8	73.0	333	7	US-11-266-748A-172240	Sequence 172240,
	23	16.8	73.0	333	7	US-11-266-748A-245535	Sequence 245535,
c	24	16.8	73.0	1147	7	US-11-266-748A-94013	Sequence 94013, A
	25	16.8	73.0	1147	7	US-11-266-748A-146824	Sequence 146824,
c	26	16.8	73.0	1781	6	US-10-953-349-35542	Sequence 35542, A
	27	16.6	72.2	487	7	US-11-266-748A-307010	Sequence 307010,
	28	16.6	72.2	1000	7	US-11-266-748A-220653	Sequence 220653,
	29	16.6	72.2	1000	7	US-11-266-748A-284005	Sequence 284005,
c	30	16.6	72.2	1000	7	US-11-266-748A-335434	Sequence 335434,
	31	16.6	72.2	1000	7	US-11-266-748A-393867	Sequence 393867,
c	32	16.6	72.2	1000	7	US-11-266-748A-464913	Sequence 464913,
c	33	16.6	72.2	1734	7	US-11-217-529-2269	Sequence 2269, Ap
	34	16.6	72.2	2906	7	US-11-266-748A-24954	Sequence 24954, A
	35	16.6	72.2	3088	6	US-10-449-902-20524	Sequence 20524, A
c	36	16.4	71.3	1050	6	US-10-471-571A-2467	Sequence 2467, Ap
	37	16.4	71.3	1322	7	US-11-216-545-1586	Sequence 1586, Ap
	38	16.4	71.3	1954	7	US-11-140-450-110	Sequence 110, App
	39	16.4	71.3	1954	7	US-11-292-951-19	Sequence 19, Appl
	40	16.2	70.4	309	7	US-11-266-748A-95119	Sequence 95119, A
c	41	16.2	70.4	309	7	US-11-266-748A-147930	Sequence 147930,
c	42	16.2	70.4	647	7	US-11-266-748A-416821	Sequence 416821,
	43	16.2	70.4	1000	7	US-11-266-748A-198331	Sequence 198331,
c	44	16.2	70.4	1209	6	US-10-449-902-1300	Sequence 1300, Ap
c	45	16.2	70.4	1216	6	US-10-449-902-3674	Sequence 3674, Ap

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:47:09 ; Search time 5.90323 Seconds
(without alignments)
8558.022 Million cell updates/sec

Title: US-08-783-734D-31
Perfect score: 27
Sequence: 1 cattaaatgatttattatcagaattgc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	20.8	77.0	966	3 US-09-134-001C-53	Sequence 53, Appl
2	20.2	74.8	1206	3 US-09-248-796A-1184	Sequence 1184, Ap
3	20.2	74.8	14602	2 US-08-597-236-1	Sequence 1, Appli
4	20.2	74.8	14602	2 US-08-746-682A-1	Sequence 1, Appli
5	19.8	73.3	1830121	3 US-09-557-884-1	Sequence 1, Appli
6	19.8	73.3	1830121	3 US-09-643-990A-1	Sequence 1, Appli

	7	19.8	73.3	1830121	3	US-10-158-865-1	Sequence 1, Appli
	8	19.6	72.6	501	3	US-09-248-796A-4330	Sequence 4330, Ap
c	9	19.6	72.6	3034	5	US-09-430-590E-102	Sequence 102, App
	10	19.6	72.6	44870	3	US-09-949-016-12554	Sequence 12554, A
	11	19.6	72.6	44881	3	US-09-949-016-16349	Sequence 16349, A
	12	19.2	71.1	372	3	US-09-248-796A-1381	Sequence 1381, Ap
c	13	19.2	71.1	2760	3	US-09-198-484-1	Sequence 1, Appli
	14	19.2	71.1	84870	3	US-09-949-016-17547	Sequence 17547, A
c	15	19	70.4	969	3	US-09-830-230A-424	Sequence 424, App
c	16	19	70.4	1020	3	US-09-830-230A-423	Sequence 423, App
c	17	19	70.4	1106	2	US-08-020-245A-2	Sequence 2, Appli
c	18	19	70.4	1106	2	US-08-396-957A-2	Sequence 2, Appli
c	19	19	70.4	2304	2	US-08-020-245A-1	Sequence 1, Appli
c	20	19	70.4	2304	2	US-08-396-957A-1	Sequence 1, Appli
	21	18.8	69.6	6507	3	US-09-949-016-15053	Sequence 15053, A
c	22	18.8	69.6	48691	3	US-09-949-016-16308	Sequence 16308, A
	23	18.6	68.9	650	3	US-09-669-751-180	Sequence 180, App
	24	18.6	68.9	816	3	US-09-270-767-13129	Sequence 13129, A
	25	18.6	68.9	44100	3	US-09-719-554-63	Sequence 63, Appl
	26	18.6	68.9	45484	3	US-09-949-016-12967	Sequence 12967, A
	27	18.6	68.9	50000	3	US-09-662-254B-23	Sequence 23, Appl
	28	18.6	68.9	132871	3	US-09-949-016-13863	Sequence 13863, A
	29	18.6	68.9	161607	3	US-09-949-016-12210	Sequence 12210, A
c	30	18.6	68.9	818128	3	US-09-949-016-14546	Sequence 14546, A
c	31	18.6	68.9	818128	3	US-09-949-016-14547	Sequence 14547, A
c	32	18.6	68.9	818128	3	US-09-949-016-14548	Sequence 14548, A
c	33	18.6	68.9	818128	3	US-09-949-016-14549	Sequence 14549, A
c	34	18.6	68.9	818128	3	US-09-949-016-14550	Sequence 14550, A
c	35	18.6	68.9	818128	3	US-09-949-016-14551	Sequence 14551, A
c	36	18.6	68.9	818128	3	US-09-949-016-14552	Sequence 14552, A
c	37	18.6	68.9	818128	3	US-09-949-016-14553	Sequence 14553, A
c	38	18.6	68.9	818128	3	US-09-949-016-14554	Sequence 14554, A
c	39	18.6	68.9	818128	3	US-09-949-016-14555	Sequence 14555, A
c	40	18.6	68.9	818128	3	US-09-949-016-14556	Sequence 14556, A
c	41	18.6	68.9	818128	3	US-09-949-016-14557	Sequence 14557, A
c	42	18.6	68.9	818128	3	US-09-949-016-14558	Sequence 14558, A
c	43	18.6	68.9	818128	3	US-09-949-016-14559	Sequence 14559, A
c	44	18.6	68.9	818128	3	US-09-949-016-14560	Sequence 14560, A
c	45	18.6	68.9	818128	3	US-09-949-016-14561	Sequence 14561, A

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-31.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:57:54 ; Search time 3.93548 Seconds
(without alignments)
8112.698 Million cell updates/sec

Title: US-08-783-734D-31
Perfect score: 27
Sequence: 1 cattaaatgatttattatcagaattgc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match Length	DB	ID	Description
	1	19.8	73.3	138443	7	US-11-266-748A-60103
c	2	19.6	72.6	480	7	US-11-266-748A-14601
c	3	19.6	72.6	1000	7	US-11-266-748A-283079
	4	19.6	72.6	1000	7	US-11-266-748A-309719
c	5	19.6	72.6	3034	7	US-11-238-031-102
c	6	19.6	72.6	4860	7	US-11-266-748A-29410
	7	19	70.4	663	7	US-11-199-489A-21
	8	19	70.4	1000	7	US-11-266-748A-204243

	9	18.8	69.6	684973	7	US-11-266-748A-32013	Sequence 32013, A
c	10	18.6	68.9	265	7	US-11-266-748A-369240	Sequence 369240,
	11	18.6	68.9	265	7	US-11-266-748A-452619	Sequence 452619,
c	12	18.6	68.9	344	7	US-11-266-748A-5696	Sequence 5696, Ap
c	13	18.6	68.9	608	7	US-11-266-748A-81406	Sequence 81406, A
	14	18.6	68.9	608	7	US-11-266-748A-134217	Sequence 134217,
c	15	18.6	68.9	958	7	US-11-266-748A-57125	Sequence 57125, A
c	16	18.6	68.9	958	7	US-11-266-748A-224637	Sequence 224637,
	17	18.6	68.9	1000	7	US-11-266-748A-200345	Sequence 200345,
	18	18.6	68.9	1000	7	US-11-266-748A-206315	Sequence 206315,
c	19	18.6	68.9	1091	7	US-11-266-748A-256695	Sequence 256695,
	20	18.6	68.9	1091	7	US-11-266-748A-317212	Sequence 317212,
	21	18.6	68.9	1337	6	US-10-953-349-22500	Sequence 22500, A
	22	18.6	68.9	1430	7	US-11-216-545-7445	Sequence 7445, Ap
c	23	18.6	68.9	1703	7	US-11-266-748A-357507	Sequence 357507,
c	24	18.6	68.9	1703	7	US-11-266-748A-386400	Sequence 386400,
	25	18.6	68.9	1703	7	US-11-266-748A-440886	Sequence 440886,
	26	18.6	68.9	56093	7	US-11-266-748A-61305	Sequence 61305, A
c	27	18.6	68.9	340000	7	US-11-266-748A-61353	Sequence 61353, A
	28	18.6	68.9	1071650	7	US-11-266-748A-22664	Sequence 22664, A
c	29	18.2	67.4	311	7	US-11-266-748A-166009	Sequence 166009,
	30	18.2	67.4	311	7	US-11-266-748A-244142	Sequence 244142,
	31	18.2	67.4	885	7	US-11-266-748A-118748	Sequence 118748,
c	32	18.2	67.4	885	7	US-11-266-748A-160912	Sequence 160912,
	33	18.2	67.4	1051	7	US-11-266-748A-85113	Sequence 85113, A
c	34	18.2	67.4	1051	7	US-11-266-748A-137924	Sequence 137924,
	35	18.2	67.4	1656	7	US-11-217-529-78831	Sequence 78831, A
c	36	18.2	67.4	3132	7	US-11-217-529-77436	Sequence 77436, A
c	37	18.2	67.4	3357	6	US-10-449-902-21840	Sequence 21840, A
	38	18.2	67.4	5040	6	US-10-449-902-24467	Sequence 24467, A
c	39	18.2	67.4	684973	7	US-11-266-748A-32013	Sequence 32013, A
c	40	18	66.7	511	7	US-11-266-748A-17986	Sequence 17986, A
c	41	18	66.7	983	7	US-11-266-748A-267502	Sequence 267502,
	42	18	66.7	983	7	US-11-266-748A-328019	Sequence 328019,
	43	18	66.7	1000	7	US-11-266-748A-212714	Sequence 212714,
	44	18	66.7	1318	7	US-11-266-748A-58178	Sequence 58178, A
	45	18	66.7	1508	6	US-10-449-902-4960	Sequence 4960, Ap

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-31.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:48:31 ; Search time 44.4624 Seconds
(without alignments)
7461.730 Million cell updates/sec

Title: US-08-783-734D-31
Perfect score: 27
Sequence: 1 cattaaatgattttattatcagaattgc 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID	Description	

1	21.8	80.7	582	4	US-09-925-065A-346391	Sequence 346391,
2	21.8	80.7	582	5	US-09-925-065A-346391	Sequence 346391,
3	21.8	80.7	632	12	US-10-301-480-209648	Sequence 209648,
4	21.8	80.7	632	12	US-10-301-480-823057	Sequence 823057,
5	21.8	80.7	634	4	US-09-925-065A-110091	Sequence 110091,
6	21.8	80.7	634	5	US-09-925-065A-110091	Sequence 110091,
7	21.8	80.7	634	12	US-10-301-480-214207	Sequence 214207,
8	21.8	80.7	634	12	US-10-301-480-827616	Sequence 827616,
c 9	21.8	80.7	638	4	US-09-925-065A-115221	Sequence 115221,
c 10	21.8	80.7	638	5	US-09-925-065A-115221	Sequence 115221,
11	20.8	77.0	966	8	US-10-724-972A-2913	Sequence 2913, Ap
c 12	20.2	74.8	536	8	US-10-424-599-128789	Sequence 128789,
c 13	20.2	74.8	600	6	US-10-027-632-226907	Sequence 226907,
c 14	20.2	74.8	600	7	US-10-027-632-226907	Sequence 226907,
c 15	19.8	73.3	544	12	US-10-301-480-518239	Sequence 518239,
c 16	19.8	73.3	544	12	US-10-301-480-1131648	Sequence 1131648,
c 17	19.8	73.3	547	4	US-09-925-065A-461262	Sequence 461262,
c 18	19.8	73.3	547	5	US-09-925-065A-461262	Sequence 461262,
c 19	19.8	73.3	600	16	US-11-052-554A-468	Sequence 468, App
c 20	19.8	73.3	729	12	US-10-301-480-536352	Sequence 536352,
c 21	19.8	73.3	729	12	US-10-301-480-1149761	Sequence 1149761,
c 22	19.8	73.3	902	12	US-10-301-480-536351	Sequence 536351,
c 23	19.8	73.3	902	12	US-10-301-480-1149760	Sequence 1149760,
24	19.8	73.3	1765	10	US-10-795-159-281	Sequence 281, App
25	19.8	73.3	302250	3	US-09-962-832-154	Sequence 154, App
c 26	19.8	73.3	302250	3	US-09-962-832-154	Sequence 154, App
27	19.8	73.3	302250	10	US-10-843-641A-6040	Sequence 6040, Ap
c 28	19.8	73.3	302250	10	US-10-843-641A-6040	Sequence 6040, Ap
29	19.8	73.3	417576	10	US-10-795-159-684	Sequence 684, App
30	19.8	73.3	1830121	8	US-10-329-670-1	Sequence 1, Appli
31	19.8	73.3	1830121	9	US-10-158-865-1	Sequence 1, Appli
32	19.8	73.3	1830121	10	US-10-981-687-1	Sequence 1, Appli
c 33	19.6	72.6	347	3	US-09-732-627A-3962	Sequence 3962, Ap
34	19.6	72.6	444	4	US-09-925-065A-5999994	Sequence 5999994,
35	19.6	72.6	444	5	US-09-925-065A-5999994	Sequence 5999994,
36	19.6	72.6	444	12	US-10-301-480-22564	Sequence 22564, A
37	19.6	72.6	444	12	US-10-301-480-635973	Sequence 635973,
38	19.6	72.6	472	6	US-10-027-632-96609	Sequence 96609, A
39	19.6	72.6	472	6	US-10-027-632-319014	Sequence 319014,
40	19.6	72.6	472	7	US-10-027-632-96609	Sequence 96609, A
41	19.6	72.6	472	7	US-10-027-632-319014	Sequence 319014,
c 42	19.6	72.6	551	3	US-09-867-701-6279	Sequence 6279, Ap
43	19.6	72.6	819	8	US-10-282-122A-34171	Sequence 34171, A
c 44	19.6	72.6	1923	10	US-10-750-185-38883	Sequence 38883, A
c 45	19.6	72.6	1923	10	US-10-750-623-38883	Sequence 38883, A

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-10.ra1.

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OM protein - protein search, using sw model

Run on: June 29, 2006, 14:22:56 ; Search time 31 Seconds
(without alignments)
2272.973 Million cell updates/sec

Title: US-08-783-734D-10
Perfect score: 4321
Sequence: 1 MMCQKFYVLLHWEFLYVIA.....IPSNVKKFYIHGMCTVLFMD 805

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	4271	98.8	894	1	US-08-599-455B-2	Sequence 2, Appli
2	4271	98.8	894	2	US-09-069-781B-2	Sequence 2, Appli
3	4271	98.8	894	2	US-08-618-957A-12	Sequence 12, Appl
4	4271	98.8	894	2	US-09-137-132-2	Sequence 2, Appli
5	4271	98.8	894	2	US-08-864-564A-2	Sequence 2, Appli
6	4271	98.8	894	2	US-09-094-410-2	Sequence 2, Appli
7	4271	98.8	894	2	US-08-708-123D-2	Sequence 2, Appli
8	4271	98.8	894	2	US-08-583-153A-2	Sequence 2, Appli
9	4271	98.8	894	2	US-08-570-142D-2	Sequence 2, Appli

10	4271	98.8	894	2	US-08-638-524B-2	Sequence 2, Appli
11	4271	98.8	894	2	US-10-095-929-12	Sequence 12, Appl
12	4271	98.8	894	2	US-09-950-149-2	Sequence 2, Appli
13	4271	98.8	1162	1	US-08-599-455B-43	Sequence 43, Appl
14	4271	98.8	1162	2	US-09-069-781B-43	Sequence 43, Appl
15	4271	98.8	1162	2	US-09-137-132-43	Sequence 43, Appl
16	4271	98.8	1162	2	US-08-864-564A-43	Sequence 43, Appl
17	4271	98.8	1162	2	US-09-094-410-43	Sequence 43, Appl
18	4271	98.8	1162	2	US-08-708-123D-43	Sequence 43, Appl
19	4271	98.8	1162	2	US-08-638-524B-43	Sequence 43, Appl
20	4271	98.8	1162	2	US-09-950-149-43	Sequence 43, Appl
21	4147	96.0	896	1	US-08-640-389A-12	Sequence 12, Appl
22	4031	93.3	783	2	US-08-780-562-7	Sequence 7, Appli
23	3991	92.4	1162	2	US-08-803-346-1	Sequence 1, Appli
24	3983	92.2	895	2	US-08-827-962-19	Sequence 19, Appl
25	3983	92.2	1162	2	US-08-827-962-15	Sequence 15, Appl
26	3977	92.0	1162	2	US-08-827-962-20	Sequence 20, Appl
27	3947	91.3	895	2	US-08-827-962-21	Sequence 21, Appl
28	3355	77.6	804	2	US-09-116-676-10	Sequence 10, Appl
29	3340	77.3	896	2	US-08-780-562-3	Sequence 3, Appli
30	3340	77.3	923	2	US-08-780-562-4	Sequence 4, Appli
31	3340	77.3	1165	1	US-08-599-455B-4	Sequence 4, Appli
32	3340	77.3	1165	2	US-09-093-814-1	Sequence 1, Appli
33	3340	77.3	1165	2	US-09-069-781B-4	Sequence 4, Appli
34	3340	77.3	1165	2	US-08-618-957A-11	Sequence 11, Appl
35	3340	77.3	1165	2	US-09-137-132-4	Sequence 4, Appli
36	3340	77.3	1165	2	US-09-094-410-4	Sequence 4, Appli
37	3340	77.3	1165	2	US-08-708-123D-4	Sequence 4, Appli
38	3340	77.3	1165	2	US-08-583-153A-4	Sequence 4, Appli
39	3340	77.3	1165	2	US-08-570-142D-4	Sequence 4, Appli
40	3340	77.3	1165	2	US-08-780-562-2	Sequence 2, Appli
41	3340	77.3	1165	2	US-08-638-524B-4	Sequence 4, Appli
42	3340	77.3	1165	2	US-10-095-929-11	Sequence 11, Appl
43	3340	77.3	1165	2	US-09-950-149-4	Sequence 4, Appli
44	3328	77.0	896	2	US-08-618-957A-10	Sequence 10, Appl
45	3328	77.0	896	2	US-09-357-914-33	Sequence 33, Appl

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-10.rapbm.

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OM protein - protein search, using sw model

Run on: June 29, 2006, 14:23:16 ; Search time 91 Seconds
(without alignments)
4097.670 Million cell updates/sec

Title: US-08-783-734D-10
Perfect score: 4321
Sequence: 1 MMCQKIFYVLLHWEFLYVIA.....IPSNVKKFYIHGMCTVLFMD 805

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4271	98.8	894	2	US-08-779-457-51
2	4271	98.8	894	4	US-10-079-625-2
3	4271	98.8	894	4	US-10-095-929-12
4	4271	98.8	894	5	US-10-921-710-51
5	4271	98.8	894	6	US-11-026-133-12
6	4271	98.8	894	6	US-11-202-330-2
7	4271	98.8	1162	4	US-10-079-625-43
8	4271	98.8	1162	6	US-11-202-330-43
9	4265	98.7	1162	4	US-10-226-579-2
10	4031	93.3	783	2	US-08-779-457-7

11	4031	93.3	783	4	US-10-214-802-7	Sequence 7, Appli
12	4031	93.3	783	5	US-10-921-710-7	Sequence 7, Appli
13	4031	93.3	783	6	US-11-192-219-7	Sequence 7, Appli
14	3355	77.6	804	3	US-09-116-676-10	Sequence 10, Appl
15	3340	77.3	896	2	US-08-779-457-3	Sequence 3, Appli
16	3340	77.3	896	4	US-10-214-802-3	Sequence 3, Appli
17	3340	77.3	896	4	US-10-373-624A-2	Sequence 2, Appli
18	3340	77.3	896	5	US-10-774-721-10	Sequence 10, Appl
19	3340	77.3	896	5	US-10-921-710-3	Sequence 3, Appli
20	3340	77.3	896	6	US-11-192-219-3	Sequence 3, Appli
21	3340	77.3	923	2	US-08-779-457-4	Sequence 4, Appli
22	3340	77.3	923	4	US-10-214-802-4	Sequence 4, Appli
23	3340	77.3	923	5	US-10-921-710-4	Sequence 4, Appli
24	3340	77.3	923	6	US-11-192-219-4	Sequence 4, Appli
25	3340	77.3	925	5	US-10-492-403A-15	Sequence 15, Appl
26	3340	77.3	1165	2	US-08-779-457-2	Sequence 2, Appli
27	3340	77.3	1165	3	US-09-894-039-1	Sequence 1, Appli
28	3340	77.3	1165	4	US-10-095-929-11	Sequence 11, Appl
29	3340	77.3	1165	4	US-10-214-802-2	Sequence 2, Appli
30	3340	77.3	1165	4	US-10-226-579-4	Sequence 4, Appli
31	3340	77.3	1165	5	US-10-921-710-2	Sequence 2, Appli
32	3340	77.3	1165	5	US-10-893-315-73	Sequence 73, Appl
33	3340	77.3	1165	6	US-11-026-133-11	Sequence 11, Appl
34	3340	77.3	1165	6	US-11-192-219-2	Sequence 2, Appli
35	3340	77.3	1165	6	US-11-202-330-4	Sequence 4, Appli
36	3333	77.1	1167	5	US-10-893-315-87	Sequence 87, Appl
37	3328	77.0	896	4	US-10-095-929-10	Sequence 10, Appl
38	3328	77.0	896	6	US-11-026-133-10	Sequence 10, Appl
39	3328	77.0	906	4	US-10-095-929-9	Sequence 9, Appli
40	3328	77.0	906	6	US-11-026-133-9	Sequence 9, Appli
41	3328	77.0	958	4	US-10-095-929-8	Sequence 8, Appli
42	3328	77.0	958	6	US-11-026-133-8	Sequence 8, Appli
43	3326	77.0	1165	4	US-10-079-625-4	Sequence 4, Appli
44	3323	76.9	960	4	US-10-095-929-3	Sequence 3, Appli
45	3323	76.9	960	6	US-11-026-133-3	Sequence 3, Appli

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-10.rapbn.

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 29, 2006, 14:23:56 ; Search time 12 Seconds
(without alignments)
1584.487 Million cell updates/sec

Title: US-08-783-734D-10
Perfect score: 4321
Sequence: 1 MMCQKFYVLLHWEFLYVIA.....IPSNVKKFYIHGMCTVLFMD 805

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 103426 seqs, 23619683 residues

Total number of hits satisfying chosen parameters: 103426

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	250.5	5.8	836	6	US-10-511-937-2988	Sequence 2988, Ap
2	194.5	4.5	422	7	US-11-296-092-32	Sequence 32, Appl
3	194.5	4.5	422	7	US-11-296-155-32	Sequence 32, Appl
4	154	3.6	368	6	US-10-449-902-38075	Sequence 38075, A
5	151	3.5	1180	6	US-10-505-928-459	Sequence 459, App
6	149	3.4	229	7	US-11-297-134-8	Sequence 8, Appli
7	149	3.4	2355	7	US-11-105-233-158	Sequence 158, App
8	136.5	3.2	635	6	US-10-511-937-2424	Sequence 2424, Ap

9	136	3.1	428	7	US-11-274-375-8	Sequence 8, Appli
10	136	3.1	629	7	US-11-274-375-10	Sequence 10, Appl
11	133.5	3.1	1998	7	US-11-348-606-3	Sequence 3, Appli
12	127	2.9	903	7	US-11-293-697-2977	Sequence 2977, Ap
13	126.5	2.9	1037	7	US-11-259-133-12	Sequence 12, Appl
14	126	2.9	337	7	US-11-274-375-2	Sequence 2, Appli
15	126	2.9	428	7	US-11-274-375-4	Sequence 4, Appli
16	126	2.9	629	7	US-11-274-375-6	Sequence 6, Appli
17	117.5	2.7	1015	7	US-11-259-133-14	Sequence 14, Appl
18	113.5	2.6	1279	6	US-10-449-902-53619	Sequence 53619, A
19	111.5	2.6	972	7	US-11-255-147-8	Sequence 8, Appli
20	111.5	2.6	972	7	US-11-248-956-5	Sequence 5, Appli
21	110.5	2.6	991	7	US-11-165-586-62	Sequence 62, Appl
22	108	2.5	650	6	US-10-509-131-11	Sequence 11, Appl
23	105	2.4	825	6	US-10-505-928-650	Sequence 650, App
24	105	2.4	825	6	US-10-511-937-3001	Sequence 3001, Ap
25	103	2.4	984	7	US-11-259-133-22	Sequence 22, Appl
26	103	2.4	1042	7	US-11-121-154-176	Sequence 176, App
27	102.5	2.4	306	6	US-10-471-571A-700	Sequence 700, App
28	102	2.4	1215	6	US-10-505-928-75	Sequence 75, Appl
29	101.5	2.3	539	7	US-11-259-133-8	Sequence 8, Appli
30	101.5	2.3	983	7	US-11-302-678-2	Sequence 2, Appli
31	101.5	2.3	983	7	US-11-259-133-6	Sequence 6, Appli
32	101.5	2.3	1650	7	US-11-175-714-70	Sequence 70, Appl
33	100.5	2.3	1134	6	US-10-449-902-51943	Sequence 51943, A
34	100	2.3	1005	7	US-11-259-133-20	Sequence 20, Appl
35	99	2.3	720	6	US-10-196-749-170	Sequence 170, App
36	99	2.3	720	7	US-11-101-316-38	Sequence 38, Appl
37	98.5	2.3	380	7	US-11-220-888-4	Sequence 4, Appli
38	98.5	2.3	380	7	US-11-331-993-2	Sequence 2, Appli
39	98.5	2.3	1204	7	US-11-289-102-236	Sequence 236, App
40	98	2.3	600	7	US-11-293-697-4457	Sequence 4457, Ap
41	97.5	2.3	310	7	US-11-220-888-1	Sequence 1, Appli
42	97.5	2.3	984	7	US-11-283-329-104	Sequence 104, App
43	97.5	2.3	1871	6	US-10-501-834-26	Sequence 26, Appl
44	97	2.2	439	7	US-11-297-134-22	Sequence 22, Appl
45	97	2.2	5635	6	US-10-766-760-2	Sequence 2, Appli

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:47:09 ; Search time 538.068 Seconds
(without alignments)
8558.022 Million cell updates/sec

Title: US-08-783-734D-9
Perfect score: 2461
Sequence: 1 gaggaatcgttctgcaaatc.....ctgtacttttcatggattag 2461

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	2433.4	98.9	3097	2 US-08-599-455B-1	Sequence 1, Appli
2	2433.4	98.9	3097	3 US-09-069-781B-1	Sequence 1, Appli
3	2433.4	98.9	3097	3 US-09-137-132-1	Sequence 1, Appli
4	2433.4	98.9	3097	3 US-08-864-564A-1	Sequence 1, Appli
5	2433.4	98.9	3097	3 US-09-094-410-1	Sequence 1, Appli
6	2433.4	98.9	3097	3 US-08-708-123D-1	Sequence 1, Appli

7	2433.4	98.9	3097	3	US-08-583-153A-1	Sequence 1, Appli
8	2433.4	98.9	3097	3	US-08-570-142D-1	Sequence 1, Appli
9	2433.4	98.9	3097	3	US-08-638-524B-1	Sequence 1, Appli
10	2433.4	98.9	3097	4	US-09-950-149-1	Sequence 1, Appli
11	2433.4	98.9	3854	2	US-08-599-455B-42	Sequence 42, Appl
12	2433.4	98.9	3854	3	US-09-069-781B-42	Sequence 42, Appl
13	2433.4	98.9	3854	3	US-09-137-132-42	Sequence 42, Appl
14	2433.4	98.9	3854	3	US-08-864-564A-42	Sequence 42, Appl
15	2433.4	98.9	3854	3	US-09-094-410-42	Sequence 42, Appl
16	2433.4	98.9	3854	3	US-08-708-123D-42	Sequence 42, Appl
17	2433.4	98.9	3854	3	US-08-638-524B-42	Sequence 42, Appl
18	2433.4	98.9	3854	4	US-09-950-149-42	Sequence 42, Appl
19	2364.6	96.1	2868	3	US-08-780-562-8	Sequence 8, Appli
20	2163.4	87.9	3495	3	US-08-827-962-17	Sequence 17, Appl
21	2163.4	87.9	3650	3	US-08-837-635-5	Sequence 5, Appli
22	2163.4	87.9	3650	3	US-08-803-346-2	Sequence 2, Appli
23	2161.8	87.8	3650	3	US-08-837-635-7	Sequence 7, Appli
24	2160.2	87.8	3650	3	US-08-827-962-16	Sequence 16, Appl
25	1692.2	68.8	3102	3	US-08-780-562-6	Sequence 6, Appli
26	1692.2	68.8	3629	3	US-08-837-635-6	Sequence 6, Appli
27	1692.2	68.8	3800	3	US-09-023-655-885	Sequence 885, App
28	1692.2	68.8	3871	2	US-08-599-455B-3	Sequence 3, Appli
29	1692.2	68.8	3871	3	US-09-069-781B-3	Sequence 3, Appli
30	1692.2	68.8	3871	3	US-09-137-132-3	Sequence 3, Appli
31	1692.2	68.8	3871	3	US-09-094-410-3	Sequence 3, Appli
32	1692.2	68.8	3871	3	US-08-708-123D-3	Sequence 3, Appli
33	1692.2	68.8	3871	3	US-08-583-153A-3	Sequence 3, Appli
34	1692.2	68.8	3871	3	US-08-570-142D-3	Sequence 3, Appli
35	1692.2	68.8	3871	3	US-08-638-524B-3	Sequence 3, Appli
36	1692.2	68.8	3871	4	US-09-950-149-3	Sequence 3, Appli
37	1692.2	68.8	4102	3	US-08-780-562-1	Sequence 1, Appli
38	1691	68.7	3004	3	US-08-780-562-5	Sequence 5, Appli
39	1690.8	68.7	2877	2	US-08-693-697-35	Sequence 35, Appl
40	1690.8	68.7	2880	2	US-08-693-697-32	Sequence 32, Appl
41	1690.8	68.7	2991	2	US-08-355-888A-6	Sequence 6, Appli
42	1690.8	68.7	2991	2	US-08-588-190-1	Sequence 1, Appli
43	1690.8	68.7	2991	2	US-08-693-697-6	Sequence 6, Appli
44	1690.8	68.7	2991	2	US-08-640-389A-1	Sequence 1, Appli
45	1690.8	68.7	2991	3	US-08-693-696-6	Sequence 6, Appli

SCORE Search Results Details for Application 08783734 and Search Result us-08-783-734d-9.rnpbm.

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OM nucleic - nucleic search, using sw model

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Run on:      June 29, 2006, 19:48:31 ; Search time 4052.66 Seconds
              (without alignments)
              7461.730 Million cell updates/sec
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Title: US-08-783-734D-9
Perfect score: 2461
Sequence: 1 gaggaatcgttctgcgaatc.....ctgtacttttcatggattag 2461

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : Published_Applications_NA_Main:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2433.4	98.9	3097	6	US-10-079-625-1	Sequence 1, Appli
2	2433.4	98.9	3097	16	US-11-202-330-1	Sequence 1, Appli
3	2433.4	98.9	3656	6	US-10-226-579-1	Sequence 1, Appli
4	2433.4	98.9	3854	6	US-10-079-625-42	Sequence 42, Appl
5	2433.4	98.9	3854	16	US-11-202-330-42	Sequence 42, Appl
6	2390.4	97.1	2679	6	US-10-278-733-14	Sequence 14, Appl
7	2364.6	96.1	2868	2	US-08-779-457-8	Sequence 8, Appli
8	2364.6	96.1	2868	6	US-10-214-802-8	Sequence 8, Appli
9	2364.6	96.1	2868	9	US-10-921-710-8	Sequence 8, Appli
10	2364.6	96.1	2868	15	US-11-192-219-8	Sequence 8, Appli
11	2165.6	88.0	3799	16	US-11-136-527-2058	Sequence 2058, Ap
12	2148.8	87.3	3489	6	US-10-278-733-18	Sequence 18, Appl
13	1692.2	68.8	3102	2	US-08-779-457-6	Sequence 6, Appli
14	1692.2	68.8	3102	6	US-10-214-802-6	Sequence 6, Appli
15	1692.2	68.8	3102	9	US-10-921-710-6	Sequence 6, Appli
16	1692.2	68.8	3102	15	US-11-192-219-6	Sequence 6, Appli
17	1692.2	68.8	3800	6	US-10-226-579-3	Sequence 3, Appli
18	1692.2	68.8	3800	8	US-10-641-643-885	Sequence 885, App
19	1692.2	68.8	3800	10	US-10-893-315-12	Sequence 12, Appl
20	1692.2	68.8	3871	16	US-11-202-330-3	Sequence 3, Appli
21	1692.2	68.8	4102	2	US-08-779-457-1	Sequence 1, Appli
22	1692.2	68.8	4102	6	US-10-214-802-1	Sequence 1, Appli
23	1692.2	68.8	4102	9	US-10-921-710-1	Sequence 1, Appli
24	1692.2	68.8	4102	15	US-11-192-219-1	Sequence 1, Appli
25	1691	68.7	3004	2	US-08-779-457-5	Sequence 5, Appli
26	1691	68.7	3004	6	US-10-214-802-5	Sequence 5, Appli
27	1691	68.7	3004	9	US-10-921-710-5	Sequence 5, Appli
28	1691	68.7	3004	15	US-11-192-219-5	Sequence 5, Appli
29	1690.8	68.7	2991	6	US-10-095-929-1	Sequence 1, Appli
30	1690.8	68.7	2991	13	US-11-026-133-1	Sequence 1, Appli
31	1689	68.6	3784	10	US-10-893-315-26	Sequence 26, Appl
32	1688.2	68.6	2415	3	US-09-116-676-9	Sequence 9, Appli
33	1687.4	68.6	3871	6	US-10-079-625-3	Sequence 3, Appli
34	1682.8	68.4	2877	6	US-10-245-616-1	Sequence 1, Appli
35	1682.8	68.4	2877	15	US-11-166-730-1	Sequence 1, Appli
36	1680.4	68.3	3909	9	US-10-014-156-12	Sequence 12, Appl
37	1676	68.1	2691	8	US-10-373-624A-1	Sequence 1, Appli
38	1676	68.1	2691	9	US-10-774-721-9	Sequence 9, Appli
39	1613.8	65.6	2751	8	US-10-373-624A-3	Sequence 3, Appli
40	1613.8	65.6	3486	8	US-10-373-624A-7	Sequence 7, Appli
41	1613.8	65.6	3486	9	US-10-774-721-13	Sequence 13, Appl
42	1613.8	65.6	3705	8	US-10-373-624A-5	Sequence 5, Appli
43	1613.8	65.6	3705	9	US-10-774-721-11	Sequence 11, Appl
44	1540	62.6	5147	6	US-10-116-802-93	Sequence 93, Appl
45	480.4	19.5	630	10	US-10-803-459C-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

This page gives you Search Results detail for the Application 08783734 and Search Result us-08-783-734d-9.rnpbn.

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OM nucleic - nucleic search, using sw model

Run on: June 29, 2006, 19:57:54 ; Search time 358.712 Seconds
(without alignments)
8112.698 Million cell updates/sec

Title: US-08-783-734D-9
Perfect score: 2461
Sequence: 1 gaggaatcgttctgcaaatc.....ctgtacttttcatggattag 2461

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 809770 seqs, 591248006 residues

Total number of hits satisfying chosen parameters: 1619540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1692.2	68.8	5157	7	US-11-266-748A-56701	Sequence 56701, A
2	1676	68.1	4968	7	US-11-266-748A-31964	Sequence 31964, A
3	1087.8	44.2	1538	7	US-11-266-748A-250506	Sequence 250506,
c 4	1087.8	44.2	1538	7	US-11-266-748A-311023	Sequence 311023,
5	554.2	22.5	756	7	US-11-266-748A-368606	Sequence 368606,
c 6	554.2	22.5	756	7	US-11-266-748A-451985	Sequence 451985,
7	338.8	13.8	1000	7	US-11-266-748A-220684	Sequence 220684,
8	338.8	13.8	1000	7	US-11-266-748A-284131	Sequence 284131,

c	9	338.8	13.8	1000	7	US-11-266-748A-335560	Sequence 335560,
	10	338.8	13.8	1000	7	US-11-266-748A-394020	Sequence 394020,
c	11	338.8	13.8	1000	7	US-11-266-748A-465066	Sequence 465066,
	12	179.4	7.3	540	7	US-11-266-748A-52634	Sequence 52634, A
	13	179.4	7.3	965	7	US-11-266-748A-250812	Sequence 250812,
c	14	179.4	7.3	965	7	US-11-266-748A-311329	Sequence 311329,
	15	116	4.7	659	7	US-11-266-748A-47098	Sequence 47098, A
	16	39	1.6	3085	7	US-11-266-748A-28955	Sequence 28955, A
	17	35.8	1.5	291	7	US-11-266-748A-8149	Sequence 8149, Ap
	18	35.6	1.4	726	6	US-10-471-571A-5187	Sequence 5187, Ap
c	19	35.2	1.4	639	7	US-11-266-748A-52821	Sequence 52821, A
c	20	35.2	1.4	722	7	US-11-266-748A-79651	Sequence 79651, A
c	21	35.2	1.4	722	7	US-11-266-748A-110622	Sequence 110622,
	22	35.2	1.4	722	7	US-11-266-748A-132462	Sequence 132462,
c	23	35.2	1.4	816	7	US-11-266-748A-163458	Sequence 163458,
c	24	35.2	1.4	907	7	US-11-266-748A-79652	Sequence 79652, A
c	25	35.2	1.4	907	7	US-11-266-748A-110623	Sequence 110623,
	26	35.2	1.4	907	7	US-11-266-748A-132463	Sequence 132463,
c	27	35.2	1.4	1527	7	US-11-266-748A-348151	Sequence 348151,
c	28	35.2	1.4	1527	7	US-11-266-748A-381638	Sequence 381638,
	29	35.2	1.4	1527	7	US-11-266-748A-431530	Sequence 431530,
c	30	35.2	1.4	1834	7	US-11-266-748A-185027	Sequence 185027,
c	31	35.2	1.4	1834	7	US-11-266-748A-192533	Sequence 192533,
	32	34.8	1.4	1474	7	US-11-266-748A-27239	Sequence 27239, A
	33	34.4	1.4	3033	7	US-11-293-697-103	Sequence 103, App
c	34	34.2	1.4	1804	6	US-10-953-349-11271	Sequence 11271, A
c	35	34	1.4	599	6	US-10-449-902-4612	Sequence 4612, Ap
	36	34	1.4	1062	6	US-10-449-902-2289	Sequence 2289, Ap
	37	34	1.4	3642	7	US-11-217-529-79570	Sequence 79570, A
	38	34	1.4	4192	7	US-11-266-748A-56124	Sequence 56124, A
c	39	33.8	1.4	1058	7	US-11-266-748A-166553	Sequence 166553,
	40	33.8	1.4	3152	7	US-11-266-748A-348490	Sequence 348490,
	41	33.8	1.4	3152	7	US-11-266-748A-381851	Sequence 381851,
c	42	33.8	1.4	3152	7	US-11-266-748A-431869	Sequence 431869,
	43	33.8	1.4	150024	7	US-11-266-748A-60141	Sequence 60141, A
	44	33.6	1.4	640	7	US-11-266-748A-41507	Sequence 41507, A
	45	33.6	1.4	992	7	US-11-266-748A-364302	Sequence 364302,